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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=16; hr=12; min=59; sec=28; ms=485;]

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Application No: 10584438

Version No: 2.0

Input Set:

Output Set:

Started: 2008-06-13 16:04:14.539

Finished: 2008-06-13 16:04:15.976

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 437 ms

Total Warnings: 20

Total Errors: 0

No. of SeqIDs Defined: 20

Actual SeqID Count: 20

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Total Errors: 0
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Kroz, Monika
 Dickneite, Gerhard
 Hauser, Hans-Peter
 Weimer, Thomas
 Sleep, Darrell

<120> Interleukin-11 fusion protein

<130> P31755 USA

<140> 10584438

<141> 2008-06-13

<150> GB 03027770.1

<151> 2003-12-03

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<223> Oligonucleotide Linker VC053

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<213> Artificial Sequence

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<223> Oligonucleotide Linker VC054

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<213> Artificial Sequence

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<210> 15

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> N-terminal IL11-albumin fusion

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<210> 16
<211> 786
<212> PRT
<213> Artificial Sequence

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<220>
<223> N-terminal IL11-albumin fusion

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Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg
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Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr
35 40 45

Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp
50 55 60

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu
65 70 75 80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu
85 90 95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp
100 105 110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu
115 120 125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu
130 135 140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala
145 150 155 160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala
165 170 175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg
180 185 190

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Gly	Leu	Leu	Leu	Leu	Lys	Thr	Arg	Leu	Asp	Ala	His	Lys	Ser	Glu	Val	195	200	205	
Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu	Glu	Asn	Phe	Lys	Ala	Leu	Val	210	215	220	
Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln	Gln	Cys	Pro	Phe	Glu	Asp	His	225	230	235	240
Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu	Phe	Ala	Lys	Thr	Cys	Val	Ala	245	250	255	
Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys	Ser	Leu	His	Thr	Leu	Phe	Gly	260	265	270	
Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu	Arg	Glu	Thr	Tyr	Gly	Glu	Met	275	280	285	
Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro	Glu	Arg	Asn	Glu	Cys	Phe	Leu	290	295	300	
Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	Leu	Pro	Arg	Leu	Val	Arg	Pro	Glu	305	310	315	320
Val	Asp	Val	Met	Cys	Thr	Ala	Phe	His	Asp	Asn	Glu	Glu	Thr	Phe	Leu	325	330	335	
Lys	Lys	Tyr	Leu	Tyr	Glu	Ile	Ala	Arg	Arg	His	Pro	Tyr	Phe	Tyr	Ala	340	345	350	
Pro	Glu	Leu	Leu	Phe	Phe	Ala	Lys	Arg	Tyr	Lys	Ala	Ala	Phe	Thr	Glu	355	360	365	
Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	Ala	Cys	Leu	Leu	Pro	Lys	Leu	Asp	370	375	380	
Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	Ser	Ser	Ala	Lys	Gln	Arg	Leu	Lys	385	390	395	400
Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	405	410	415	
Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	Lys	Ala	Glu	Phe	Ala	Glu	Val	420	425	430	
Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	Val	His	Thr	Glu	Cys	Cys	His	435	440	445	
Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	Arg	Ala	Asp	Leu	Ala	Lys	Tyr	450	455	460	
Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	Ser	Lys	Leu	Lys	Glu	Cys	Cys	465	470	475	480
Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	Cys	Ile	Ala	Glu	Val	Glu	Asn	485	490	495	

<210> 17
 <211> 762
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Mature N-terminal IL11-albumin fusion

 <400> 17
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 20 25 30

 Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His
 35 40 45

 Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly
 50 55 60

 Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu
 65 70 75 80

 Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser
 85 90 95

 Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp
 100 105 110

 Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro
 115 120 125

 Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser
 130 135 140

 Ala Trp Gly Gly Ile Arg Ala Ala His Ala Ile Leu Gly Gly Leu His
 145 150 155 160

 Leu Thr Leu Asp Trp Ala Val Arg Gly Leu Leu Leu Leu Lys Thr Arg
 165 170 175

 Leu Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
 180 185 190

 Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
 195 200 205

 Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
 210 215 220

 Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
 225 230 235 240

 Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
 245 250 255

Leu	Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	260	265	270
Pro	Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	275	280	285
Leu	Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	290	295	300
His	Asp	Asn	Glu	Glu	Thr	Phe	Leu	Lys	Lys	Tyr	Leu	Tyr	Glu	Ile	Ala	305	310	315
Arg	Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro	Glu	Leu	Leu	Phe	Phe	Ala	Lys	325	330	335
Arg	Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	340	345	350
Ala	Cys	Leu	Leu	Pro	Lys	Leu	Asp	Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	355	360	365
Ser	Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	370	375	380
Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	385	390	395
Pro	Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	405	410	415
Lys	Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	420	425	430
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His	Cys	Ile	Ala	Glu	Val	Glu	Asn	Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	465	470	475
Ser	Leu	Ala	Ala	Asp	Phe	Val	Glu	Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	485	490	495
Ala	Glu	Ala	Lys	Asp	Val	Phe	Leu	Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	500	505	510
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